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GENETIC VARIABILITY, HERITABILITY AND CORRELATION STUDIES IN APPLE (*Malus* × *domestica* BORKH) CULTIVARS OF KASHMIR VALLEY

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ABSTRACT

Present study has been carried out to access the genetic variability and heritability between various cultivars of Kashmir valley of India. In present study, 40 apple cultivars were selected and various characters like fruit length, fruit diameter, fruit weight, fruit firmness, leaf blade length and width, petiole length, pedicel length, TSS and acidity were measured using standard procedures. The results of study revealed a huge genetic variation among the various studied characters. Highest heritability estimate (99.5%) was found for fruit weight followed by fruit length (98.5%). Similarly expected genetic advance was highest for fruit weight (55.84%) followed by acidity (42.69%) and least for TSS (13.13%). It was found that correlation between fruit length and fruit weight was reported maximum, this was followed by fruit diameter, these treatments were found statistically significant ($p<0.05$). While performing cluster analysis, it was found that 36 cultivars lie within cluster-I, 3 in Cluster-II and cluster-III was monogenic containing only one cultivar i.e. Scarlet Siberian. Average intra and inter cluster distance (D^2) value revealed that the cluster I had the highest intra cluster distance (119.95) followed by cluster II (83.89). Inter cluster distance was maximum between cluster I and Cluster III (1521.46) followed by cluster I and cluster II 9745.61).Cluster I had maximum mean values for fruit length (67.48 mm), fruit diameter (72.47 mm), fruit weight (156.10 g) and petiole length (28.83 mm). While the cluster II is characterized by highest leaf length (88.11 mm), leaf width (55.00 mm), acidity (0.26%) and lowest fruit firmness (5.86 kg/cm^2), pedicel length (19.78 mm) and TSS (10.97 ºBrix). Cluster III had maximum mean values for fruit firmness (9.43 kg/cm^2), pedicel length (31.00 mm), TSS (14.23 ºBrix). Fruit weight was main factor contributing towards divergence (54.10%) followed by acidity (12.30%) and least contributing factor was TSS (0.26%).

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1 Introduction

Apple is the most ubiquitous fruit in temperate regions and it has been cultivated throughout Europe and Asia since antiquity (Janick et al., 1996)). Apple was introduced into India by the British in the Kullu Valley of Himachal Pradesh as far back as 1865, while the coloured delicious cultivars of apple were introduced to Shimla hills in 1917. Jammu and Kashmir contributes 75% of countries apple production (NHB, 2017). It accounts for 43.30 per cent of total area under fruits and 80.18 per cent of total fruit production in Jammu and Kashmir. It is major cash crop and is the backbone of economy in the state. It is grown in almost all the districts of Kashmir valley, in an area of 1.63 Lakh hectares with annual production of 18.6 Lakh MT with a productivity of 11.4 T/Ha (Anonymous, 2018). Although farmers grow only few varieties like Delicious strains, Maharaji, American Apirouge, Chemura, Ambrietc, but there exists tremendous diversity in apple germplasm in the departmental and university orchards that remains to be exploited.

Maintenance of genetic diversity are important for future breeding because genetic diversity gives the ability to adapt the changing environments and provide the raw material to breed new cultivars via hybridization (Doebley et al., 2006) or selection (Dzhangaliev, 2003). Estimating genetic diversity and determining the relationships among various germplasm collections enhances efficiency of its management and genetic improvement (Geleta et al., 2005). Heritability estimate provides information regarding the amount of transmissible genetic variation to total variation and determines genetic improvement and response to selection. It also suggests the relative role of genetic factors in expression of phenotypes and acts as an index of transmissibility of particular trait into its off springs however; knowledge of heritability alone does not help in formulating concrete breeding programme. Multivariate statistical techniques, which simultaneously analyze multiple measurements on each individual under investigation, are widely used in analysis of genetic diversity irrespective of whether it is morphological, biochemical, or molecular marker-based (Bhandari et al., 2017**)**. Among the multivariate techniques, cluster analysis and Principal Component Analysis (PCA) are most commonly employed (Mohammadi & Prasanna, 2003). Multivariate analysis has been frequently used for genetic diversity analysis in many fruit crops such as peach (Nikolic et al., 2010), cherry (Bhat et al., 2017), plum (Bhat et al., 2018a), Strawberry (Mishra et al., 2015), Almond (Sharma et al., 2012), Walnut (Dogra et al., 2018) and Apple (Bhat et al., 2018b). Considering the importance of apple in Kashmir, study of genetic diversity and information on relationships among native old varieties and new types would be desirable in order to allow for better management and preservation of genetic resources and their utilization within plant breeding programs. Therefore, present study has been carried out to explore the genetic variability and heritability between various cultivars of Kashmir valley of India.

2 Material and Methods

Forty apple cultivars were selected for the present study (Table 1). The study sample consists of mixture of varieties comprising of old cultivars (15), SKUAST-K released cultivars (7), newly introduced cultivars (12) and scab resistant selections (6). The characters like fruit length, fruit diameter, fruit weight, fruit firmness, leaf blade length and width, petiole length, pedicel length, TSS and acidity were measured using standard procedures.

2.1 Estimation of Genetic parameter estimates

2.1.1 Genotypic variance

Genotypic variance was calculated using the method suggested by Johnson et al. (1955).

$$\hat{\sigma}^2_g = \frac{MSG - MSE}{r}$$

Where as

$\hat{\sigma}^2_g$ = Genotypic variance,
MSG = mean sum of squares due to genotypes,
MSE = mean sum of squares due to error and
R = number of replications

Table 1 Apple germplasm studied

Group	Cultivar	Total
Released cultivars of SKUAST (K)	LalAmbri, Sunhari, Firdous, Shireen, Akbar, Shalimar Apple-1 and Shalimar Apple-2.	7
Newly introduced cultivars of SKUAST (K)	Wiltons Star, Fuji Zhen Aztec, Super Chief, Gala Redlum, Red Velox, Silver Spur, Gala Mast, Mollies Delicious, Granny Smith, Braeburn, Oregon spur and Golden Delicious Reinders.	12
Old cultivars	Red Delicious, Chamure, Maharaji, Cox Orange Pippin, American Apirouge, June Eating, Lord Lambourne, Red Gold, Benoni, Golden Delicious, Starkrimson, Yellow Newton, Scarlet Siberian, Ambri and Irish Peach.	15
Scab resistant selections	ASP-1, ASP-3, ASP-4, ASP-10, ASP-12 and ASP-69.	6
Total		40

2.1.2 Phenotypic variance

Phenotypic variance was calculated as per the procedure given by Johnson et al. (1955).

$$\hat{\sigma}^2 p = \hat{\sigma}^2 g + \hat{\sigma}^2 e$$

Where as

$\hat{\sigma}^2 p$ = Phenotypic variance
$\hat{\sigma}^2_g$ = genotypic variance and
$\hat{\sigma}^2 e$ = error variance

2.1.3 Phenotypic and genotypic co-efficient of variation

The magnitude of phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) existing in a trait was worked out by the formula given by Burton (1952):

$$PCV = \frac{\sqrt{\hat{\sigma}^2 p}}{\bar{x}} x\,100$$

Where as

$\hat{\sigma}^2 p$ = Phenotypic variance and
$\bar{x}$ = mean of the trait studied

$$GCV = \frac{\sqrt{\hat{\sigma}^2 g}}{\bar{x}} x\,100$$

Where as

$\hat{\sigma}^2_g$ = Genotypic variance and
$\bar{x}$ = mean of the trait studied

2.2 Estimation of heritability genetic advance and expected genetic gain

2.2.1 Heritability (broad sense)

It was estimated as per the procedure presented by Burton & De vane (1953), Johnson et al. (1955) and Hanson et al. (1956).

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p}$$

Where as

h^2 = Estimate of heritability in broad sense,
$\sigma^2 g$ = Genotypic variance and
$\sigma^2 p$ = Phenotypic variance

2.2.2 Genetic advance

Genetic advance at 5 per cent selection intensity was worked out by using the formula given by Lush (1949) and Johnson et al. (1955).

$$GA = \frac{\sigma^2 g}{\sigma^2 p} \times (\sigma^2 p) \times K$$

Where as

GA = Genetic advance of the trait,
$\sigma^2 g$ = genotypic variance of the trait,
$\sigma^2 p$ = phenotypic variance of the trait and
K = selection differential
(K= 2.06 at 5 per cent selection intensity)

2.2.3 Expected genetic gain (genetic advance as per cent of mean)

It was estimated as per the method suggested by Johnson et al. (1955).

$$\text{Genetic gain} = \frac{GA}{\bar{x}} \times 100$$

Where as

G.A. = Genetic advance of the trait and
$\bar{x}$ = mean of the trait

2.3 Estimation of genotypic co-variances and correlation coefficients

Covariance analysis followed the same pattern as the variance analysis. The genotypic and phenotypic covariances between two characters were obtained in the same fashion as corresponding variances. Estimation of genotypic and phenotypic variances and covariances were substituted by the formula suggested by Panse & Sukatme (1985) to calculate correlation co-efficient between all possible pairs of characters.

2.3.1 Genotypic correlation co-efficient

$$r_{xy}(g) = \frac{\hat{\sigma}^2 xy(g)}{\sqrt{\hat{\sigma}^2 x(g)\hat{\sigma}^2 y(g)}}$$

2.3.2 Phenotypic correlation coefficient

$$r_{xy}(p) = \frac{\hat{\sigma}^2 xy(p)}{\sqrt{\hat{\sigma}^2 x(p)\hat{\sigma}^2 y(p)}}$$

$r_{xy}(g), r_{xy}(p)$ = Genotypic and phenotypic correlation coefficients, respectively, between a pair of characters x and y

$\hat{\sigma}^2 xy(g), \hat{\sigma}^2 xy(p)$ = Genotypic and phenotypic covariances, respectively, for a pair of characters x and y

$\hat{\sigma}^2 x(g), \hat{\sigma}^2 y(g)$ = Genotypic variance for characters x and y, respectively and

$\hat{\sigma}^2 x(p), \hat{\sigma}^2 y(p)$ = Phenotypic variance for character x and y, respectively.

Table 2 Analysis of Variance (ANOVA) for various traits in various apple cultivars

S. No.	Source of variation	d.f	Fruit length (mm)	Fruit diameter (mm)	Fruit weight (g)	Fruit firmness (kg/cm^2)	Leaf blade length (mm)	Leaf blade width (mm)	Petiole length (mm)	Pedicel length (mm)	TSS (^oBrix)	Acidity (%)
1.	Replications	2	1.40**	0.69**	1.43**	0.03**	7.75**	14.23**	8.40**	1.97**	0.31**	0.00036**
2.	Genotypes	39	376.98**	338.43**	4673.15**	2.44**	242.53**	131.26**	77.51**	70.60**	2.73**	0.0073**
3.	Error	78	1.87	2.87	7.52	0.083	9.56	5.70	5.22	1.65	0.194	0.000294

*Significant at 0.05 probability level; **Significant at 0.01 probability level

Table 3 Estimates of mean, range, phenotypic variance, genotypic variance, phenotypic and genotypic. Coefficient of variation, heritability (bs) and genetic advance (as % of mean) for different quantitative traits in apple cultivars

S. No.	Parameters	Mean	Range	Phenotypic variance (σ^2p)	Genotypic variance (σ^2g)	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Heritability (h^2 bs)	Genetic advance (%age of mean)
1.	Fruit length (mm)	64.78	28.1-85.26	126.91	125.03	17.38	17.26	0.98	35.29
2.	Fruit diameter (mm)	69.93	30.03-85.06	114.73	111.85	15.31	15.12	0.97	30.75
3.	Fruit weight (g)	145.13	14.06-202.73	1562.73	1555.2	27.23	27.17	0.99	55.84
4.	Fruit firmness (kg/cm^2)	7.85	5.33-9.43	0.86	0.78	11.86	11.27	0.90	22.09
5.	Leaf blade length (mm)	86.21	58.66-101.00	87.22	77.65	10.83	10.22	0.89	19.86
6.	Leaf blade width (mm)	53.19	36.00-67.66	47.55	41.85	12.96	12.16	0.88	23.50
7.	Petiole length (mm)	28.52	17.66-40.33	29.32	24.09	18.98	17.20	0.82	32.13
8.	Pedicel length (mm)	26.67	15.00-38.00	24.63	22.98	18.60	17.97	0.93	35.76
9	TSS (^oBrix)	13.02	10.76-14.93	1.04	0.84	7.84	7.07	0.81	13.13
10.	Acidity (%)	0.22	0.12-0.33	0.003	0.002	23.31	21.98	0.88	42.69

3. Results and Discussion

3.1Analysis of variance

Analysis of variance for various traits under study is presented in Table 2. The data revealed significant variation among all the cultivars for all the studied traits during the programme. Mean sum of squares due to cultivars for all the traits was found highly significant. Similar results were reported by Sarkar et al. (1991) while estimating the genetic variability in litchi and the results were also in agreement with Mir (2015) in wild apple.

3.2 Variability and genetic components of variation

The genetic variability estimates including genotypic mean, range, genotypic variance (GV), phenotypic variance (PV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance as a percent of mean were estimated for each traits presented in Table 3. Perusal of Table 3 revealed that the estimates of phenotypic variance were higher than the corresponding estimates of genotypic variance. The magnitude of phenotypic and genotypic coefficient of variation was low (<10 per cent) only for TSS whereas it was moderate (10-30 per cent) for fruit length, fruit diameter, fruit weight, fruit firmness acidity, leaf blade length, leaf blade width, petiole length and pedicel length. Further, phenotypic and genotypic variance was highest for fruit weight (1562.73 and 1555.2 respectively) followed for fruit length (126.91 and 125.03) and minimum for acidity (0.003 and 0.002). Phenotypic and genotypic coefficients of variation were highest for fruit weight (27.23% and 27.17% respectively) and lowest for TSS (7.84% and 7.07%). Generally phenotypic coefficient of variation and genotypic coefficient of variation are similar with phenotypic coefficient slightly higher than genotypic coefficient of variation which indicates environmental effect in the expression of traits under observation. This was in agreement with the study of Bandale et al. (2006) and Chattopadhay et al. (2011).

3.3 Heritability and Genetic Gain

Heritability estimates (broad sense) and expected genetic gain were calculated for all observed traits (Table 3). Estimates of heritability were classified into three distinct classes with value >60.0 per cent as high heritability, >30.0 ≤ 60.0 as medium and < 30.0 per cent as low. Estimates were high for all the observed traits. Highest heritability estimate (99 per cent) was found for fruit weight followed by for fruit length (98 per cent) and lowest heritability estimate was observed for TSS (81%). Genetic advance was estimated at 5 per cent of selection intensity and converted into expected genetic gain (per cent of mean). Estimates of genetic gain were classified into three distinct classes with value >30.0 per cent as high genetic gain, >10≤30 per cent as medium and < 10.0 per cent as low genetic gain. The result revealed that the expected genetic gain was high for fruit weight (55.84 per cent) followed by acidity (42.69 per cent), pedicel length (35.76 per cent), fruit length (35.29 per cent), petiole length (32.13 per cent), fruit diameter (30.75 per cent) and medium for leaf blade width (23.50 per cent), fruit firmness (22.09 per cent), leaf blade length (19.86 per cent) and least for TSS (13.13 per cent).

Heritability (broad sense) estimates are more informative as they indicate the relative importance of genotype and environmental contribution to the variability exhibited. High heritability accompanied with greater genetic advance revealed that these characters had additive gene effect and therefore have more role in proficient selection. The results were supported by Sharma et al. (2004) who reported high heritability with high genetic gain for different parameters in apple and Sharma & Sharma (2007) who reported high heritability and genetic gain for Gala variety of apple. The results of present study were also supported by Mir (2015), Kumar & Mir (2012) and Hajnajari et al. (2012). However in present study some traits have low heritability and genetic advance which may be due to non-additive gene action associated with epitasis and dominance because traits having high heritability value together with high genetic advance are, by and large, controlled by additive gene effects (Panse, 1957).

3.4 Correlation coefficient

Correlation coefficient for various traits was estimated and presented in Table 4. The results revealed that fruit length had a significantly positive correlation with fruit diameter, fruit weight, fruit firmness, pedicel length, leaf length, leaf width, petiole length, TSS and negative correlation of fruit length was observed with acidity. Similarly fruit diameter had positive correlation with fruit length, fruit weight, fruit firmness, pedicel length, leaf blade length, leaf blade width, petiole length, TSS and negative correlation with acidity. Fruit weight showed positive correlation with fruit length, fruit diameter, fruit firmness, pedicel length, leaf blade length, leaf blade width, petiole length, TSS and negative correlation with acidity. Regarding the fruit firmness it was observed that fruit firmness was positively correlated with fruit length, fruit diameter, fruit weight, pedicel length, TSS, acidity and negatively correlated with leaf blade length, leaf blade width and petiole length, pedicel length was positively correlated with TSS and other parameters excluding acidity with which it was negatively correlated. Similarly petiole length was positively correlated with pedicel length and negatively correlated with TSS and acidity. Leaf blade length and width were positively correlated. TSS and acidity were negatively correlated. Similar correlation results between fruit length and diameter were recorded by Kumar & Srivastava (1983). The significant positive

Table 4 Estimates of genotypic (above diagonal) correlation coefficients among different traits in various apple cultivars

S. No.	Parameters	Fruit length (mm)	Fruit diameter (mm)	Fruit weight (g)	Fruit firmness (kg/cm^2)	Leaf blade length (mm)	Leaf blade width (mm)	Petiole length (mm)	Pedicel length (mm)	TSS (^{o}Brix)	Acidity (%)
1.	Fruit length (mm)	-	0.9093**	0.9217**	0.2505*	0.2946*	0.2235*	0.3472**	0.3584**	0.2193*	-0.3060**
2.	Fruit diameter (mm)		-	0.8641**	0.1794	0.2866*	0.2923*	0.3094**	0.2017*	0.1707	-0.1403
3.	Fruit weight (g)			-	0.2966*	0.3171**	0.2307*	0.3638**	0.3346**	0.2901*	-0.2692*
4.	Fruit firmness (kg/cm^2)				-	-0.2996*	-0.0877	-0.0877	0.1160	0.4149**	0.0907
5.	Leaf blade length (mm)					-	0.5242**	0.5009**	0.0766	0.0317	0.0011
6.	Leaf blade width (mm)						-	0.1056	-0.2145*	0.0738	0.1539
7.	Petiole length (mm)							-	0.2564*	-0.0038	-0.1177
8.	Pedicel length (mm)								-	0.2059*	-0.3223**
9.	TSS (^{o}Brix)									-	-0.4867**
10.	Acidity (%)										-

*, ** = Significant at 5% and 1% respectively

correlation between different characters could be useful for genetic improvement of various traits. Shin et al. (1986) observed positive association with leaf characters i.e. leaf area, weight and dry leaf weight. Klossowski (1976) between shoot length and yield, Shin et al.(1986) for leaf area with fruit length, Lauri et al.(1996) for fruit set and leaf area. Verma et al. (2002) observed significant positive correlations for characters like tree height, tree spread, fruit set, fruit weight and fruit size. Islam et al. (2010) reported strong positive correlation between yield per plant and individual fruit weight, stone weight, fruit length, fruit breadth and pulp-stone ratio in ber. The varied positive and negative correlations obtained in the present study may be attributed to the genetic make-up of the studied cultivars, varied agro-climates condition, site; orchard management practices individually or collectively may have influenced the performance of cultivar and the resultant correlations.

3.5 Cluster analysis

Based on the studied characters, whole set of apple germplasm were grouped into 3 clusters (Table 5) as per Mahalanobis D^2 analysis employing Toucher's method (Rao, 1952). Table 5 summarizes that maximum number of genotypes fall in cluster I (36) followed by cluster II (3) and cluster III (1). In addition to grouping of selections into different clusters, non-hierarchical analysis was also performed to identify the diverse and desirable selections in terms of inter cluster distance and mean performance of clusters for various characters respectively. The average intra and inter cluster distance (D^2) values revealed that the cluster I had the highest intra cluster distance value of 119.95 followed by cluster II (83.89) (Table 6). The inter cluster distance was highest between cluster I and cluster III (1521.46) followed by inter cluster distance between cluster I and cluster II (745.61). Therefore cluster I and III were most divergent with maximum inter cluster distance.

The cluster means for different characters are given in Table 7. Cluster I had maximum mean values for fruit length (67.48 mm), fruit diameter (72.47 mm), fruit weight (156.10 g) and petiole length (28.83 mm). Cluster II is characterized by highest leaf length (88.11 mm), leaf width (55.00 mm), acidity (0.26%) and lowest fruit firmness (5.86 kg/cm^2), pedicel length (19.78 mm) and TSS (10.97 ºBrix). Cluster III had maximum mean values for fruit firmness (9.43 kg/cm^2), pedicel length (31.00 mm), TSS (14.23 ºBrix) and lowest mean value for fruit length (28.10 mm), fruit diameter (30.03 mm), fruit weight (14.07 g), leaf length (58.67 mm), leaf width (36.00 mm), petiole length (18.67 mm) and fruit acidity (0.21%) (Table 7). The results clearly indicate

Table 5 Distribution of apple genotypes into clusters based on D^2 Statistics

S. No.	Cluster	No. of genotypes	Name of the cultivar
1.	I	36	Maharaji, ASP-12, Fuji Zhen Aztec, Firdous, Yellow Newton, Gala Redlum, Akbar, Mollies Delicious, Red Delicious, Super Chief, Sunhari, Golden Delicious, Oregon Spur, Shireen, Golden Delicious Reinders, Shalimar Apple-2,Wiltons Star, Starkrimson, Red Velox, Braeburn, Lord Lambourne, ASP-1, Shalimar Apple-1, Silver Spur, Ambri, ASP-3, Granny Smith, Red Gold,ASP-4,ASP-10,Gala Mast, Chamure, AmercianApirouge, Cox's Orange Pippin, ASP-69, LalAmbri,
2.	II	3	June Eating, Benoni and Irish Peach
3.	III	1	Scarlet Siberean

Table 6 Average intra cluster (Diagonal) and inter cluster (Above Diagonal) Distance Values in various apple genotypes

S. No.	Cluster	I	II	III
1.	I	119.95	745.61	1521.46
2.	II	-	83.89	394.36
3.	III	-	-	0.00

Table 7 Cluster means for various characters in different clusters of various apple genotypes

S. No.	Cluster	Fruit length (mm)	Fruit diameter (mm)	Fruit weight (g)	Fruit firmness (kg/cm^2)	Leaf blade length (mm)	Leaf blade width (mm)	Petiole length (mm)	Pedicel length (mm)	TSS (ºBrix)	Acidity (%)
1.	I	67.48	72.47	156.10	7.98	86.82	53.52	28.83	27.13	13.16	0.22
2.	II	44.67	52.89	57.23	5.86	88.11	55.00	28.11	19.78	10.97	0.26
3.	III	28.10	30.03	14.07	9.43	58.67	36.00	18.67	31.00	14.23	0.21

Table 8 Per cent contribution of individual traits towards total genetic divergence

S. No.	Traits	Times ranked 1st	Contribution (%)
1.	Fruit length (mm)	72	10.23
2.	Fruit diameter (mm)	43	6.51
3.	Fruit weight (g)	422	54.10
4.	Fruit firmness (kg/cm^2)	15	1.92
5.	Leaf blade length (mm)	31	4.17
6.	Leaf blade width (mm)	12	1.54
7.	Petiole length (mm)	9	1.15
8.	Pedicel length (mm)	60	7.82
9.	TSS (^{o}Brix)	2	0.26
10.	Acidity (%)	96	12.30

that hybridization between the cultivars from cluster I and cluster III can be utilized for getting the superior recombinants in segregating generations. Cluster means for various morpho-taxonomic and quality related characters revealed that substantial variability existed for all the traits and identified the traits to be chosen for hybridization. The results were in conformity with the Pereira et al. (2003), Saran et al. (2007), Sharma et al. (2015) and Bhat & Dhillon (2015).

The per cent contribution of the traits towards total divergence (Table 8) revealed that fruit weight was the main factor contributing towards divergence (54.10%) followed by acidity (12.30%), fruit length (10.23%) and pedicel length (7.82%). The minimum contribution towards divergence was from TSS (0.26%).The traits contributing maximum towards the divergence should be given great emphasis for deciding the clusters to be chosen for hybridization and the subsequent selection of the parents from the clusters be based on their performance (De et al. 1988).

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